Tany 1635

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/830,703**

DATE: 08/30/2001
TIME: 06:40:43

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\08302001\I830703.raw**

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 4 <110> APPLICANT: Biofrontera Pharmaceuticals AG
 5        Lubbert, Hermann
 7 <120> TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
 8        NEURODEGENERATIVE DISEASES
10 <130> FILE REFERENCE: STERN1.001APC
12 <140> CURRENT APPLICATION NUMBER: 09/830,703
13 <141> CURRENT FILING DATE: 2001-04-26
15 <150> PRIOR APPLICATION NUMBER: EP 99116766.9
16 <151> PRIOR FILING DATE: 1999-08-30
18 <160> NUMBER OF SEQ ID NOS: 34
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 3255
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
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30 cggtgaccat gatagtgttt gtcaggttca actccagcta tggcttccca gtggaggtcg 180
31 attctgacac cagcatcttg cagctcaagg aagtggttgc taagcgacag ggggttccag 240
32 ctgaccagct gcgtgtgatt tttgccggga aggagcttcc gaatcacctg acggttcaaa 300
33 actgtgacct ggaacaacag agtattgtac acatagtaca gagaccacgg aggagaagtc 360
34 atgaaacaaa tgcatctgga ggggacgaac cccagagcac ctcagagggc tccatatggg 420
35 agtccaggag cttgacacga gtggacctga gcagccatac cctgccggtg gactctgtgg 480
36 ggctggcggt cattctggac acagacagta agagggattc agaagcagcc agaggtccag 540
37 ttaaacccac ctacaacagc tttttcatct actgcaaagg ccctgccac aaggtccagc 600
38 ctggaaagct ccgagttcag tgtggcacct gcaaacaagc aaccctcacc ttggcccagg 660
39 gcccatcttg ctgggacgat gtcttaattc caaaccggat gagtggtgag tgccagtctc 720
40 cagactgccc tggaaccaga gctgaatttt tctttaaatg tggagcacac ccaacctcag 780
41 acaaggacac gtcggtagct ttgaacctga tcaccagcaa caggcgcagc atcccttgca 840
42 tagcgtgcac agatgtcagg agccctgtcc tggtcttcca gtgtaaccac cgtcacgtga 900
43 tctgtttgga ctgtttccac ttgtattgtg tcacaagact caacgatcgg cagtttgtcc 960
44 acgatgctca acttggctac tccctgccgt gtgtagctgg ctgtcccaac tccctgatta 1020
45 aagagctcca tcacttcagg atccttggag aagagcagta cactaggtac cagcagtatg 1080
46 gggccgagga atgcgtgctg caaatgggag gtgtgctgtg cccccgtcct ggctgtggag 1140
47 ctggactgct acctgaacag ggccagagga aagtcacctg cgaagggggc aacggcctgg 1200
48 gctgcgggtt tgttttctgc cgggactgta aggaagcata ccatgaaggg gattgcgact 1260
49 cactgctcga accctcagga gccacttctc aggcctacag ggtggacaaa agagccgctg 1320
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52 cccagtgcaa gctggagtgg tgctggaact gtggctgtga gtggaaccga gcctgcatgg 1500
53 gagatcactg gtttgacgtg tagagagaga tgtcacttgg ccctggacgc acaacctcaa 1560
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56 tagggcaccc acagaaaacc acagcacccg ctggccccag ggggaggagg cactttcagc 1740
57 ctctggctca ctcgaatgtc agagcttaga tgagggtgca cctttggttt ggattctgta 1800
58 gaagccatga gtgaggtggg aagtgttttc cagggttgtt gccacgccct gggtaagtaa 1860
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60 atcatctatt cccaaagggc cccctgcagt agtcaaaact atttgtttat cccccaaat 1980
61 cctatcttta caaatggtgc tgatgagatt acaacccctc tgtgtactaa tcagcttatc 2040
62 aaccaagtga gaacctagga aagctaattg gatggcagac tgcttaaatc gcagggagga 2100
63 ctcagaagcc aaacctactt ccgttcgttt cattatctgc aactttagaa agaaatgatc 2160
64 ttttttttccc cctgaaaaga taacaaagtc tgcaatttgg tttggagtat tcctactgca 2220
65 gcctggaagt ttagcttcac tgtgaattta acagagaaag tgcctataaa gggggcgttt 2280
66 ttaagagaca atcccatgat gctgcgccaa tgctaacaac agggtcaaga aacacaatgt 2340
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68 agtggggaca cctctgcata tctgctccct cctctgctgt taagccccag ggagccccat 2460
69 ccacccagtg gtcctacaga cagggcaata cacacacacc aagatagcct tcagatcaac 2520
70 atgcatcaca ctcaagtgtt aatctttcaa ggtttctttt tcttttttcct gttttttatt 2580
71 tgttttgctt ttgcttttttt tttttttttt tttggtggtg gtggggctac caaacttgag 2640
72 gcctagagct aaaaatcata tagaaatgat gttatcttgt ggtgtgagga aaggccagct 2700
73 ggcctaagtt cacacttttg tcccagtggc cctagactcc acccagccag ctcccaaaat 2760
74 gaaaagacca cctgtcaagc agcagtcagg agtctgatgt cacccatcac tatttttttt 2820
75 ccatcattgt gcttgcctct gcctccttcc acaccgtgt dacgtaatcg cattgggaag 2880
76 ccaggacaat gtttgctgtt ctgctttggg taaagggact ccctgaagct ctgtggctct 2940
77 ccagtatggt cccttttcct tcctaacaga tgcatatgtt ttcttcagaa tacaatagtg 3000
78 attcttaaaa taacccaaaa gacaggcatc cacagtgtgt gagcatgaat cacagcctgc 3060
79 attgtgtgag tgtgaatagt gggataaaag tggatgtcag aagagtggaa atcaaacctc 3120
80 tgcaaagcaa tctttctctt tctgtgaagt gtattaagaa atacctgaag tctgtgtgtg 3180
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85 <211> LENGTH: 1459
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87 <213> ORGANISM: Mus musculus
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92 tgatagtgtt tgtcaggttc aactccagct atggcttccc agtggaggtc gattctgaca 180
93 ccagcatctt gcagctcaag gaagtggttg ctaagcgaca gggggttcca gctgaccagc 240
94 tgcgtgtgat ttttgccggg aaggagcttc cgaatcacct gacggttcaa aactgtgacc 300
95 tggaacaaca gagtattgta cacatagtac agagaccacg gaggagaagt catgaaacaa 360
96 atgcatctgg aggggacgaa ccccagagca cctcagaggg ctccatatgg gagtccagga 420
97 gcttgacacg agtggacctg agcagccata ccctgccggt ggactctgtg gggctggcgg 480
98 tcattctgga cacagacagt aagagggatt cagaagcagc cagaggtcca gcagttaaac 540
99 ccacctacaa cagcttttttc atctactgca aaggcccctg ccacaaggtc cagcctggaa 600
100 agctccgagt tcagtgtggc acctgcaaac aagcaacccct caccttggcc cagggcccat 660
101 cttgctggga cgatgtctta attccaaacc ggatgagtgg tgagtgccag tctccagact 720
102 gccctggaac cagagctgaa tttttctttta aatgtggagc acacccaacc tcagacaagg 780
103 acacgtcggt agctttgaac ctgatcacca gcaacaggcg cagcatccct tgcatagcgt 840
104 gcacagatgt cagtcatctt cctctgtcat ctggtgcctc cgtgtggact cggcctcatc 900
105 tccactgaac cttgttcttt aggactgtgc aataggtcgt cacctcctac tgagaacaag 960
106 gcagcttctg gtctcttggt ttccttgctt ccaacggcag cattgactgt acacccttca 1020
107 gtcctaccaa ccccattacc tggttgattt ctttaccgct tagcttctcc aagatgccta 1080
108 tttccacaca cagtttcttg tcttccccat cccccatag gtttatgcgc atgagtaagc 1140
109 accgcacctc atgagtttgt gcttctgata caagacttcc tgggatcccc gcttgagccc 1200
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111 tcttgggctg gtgagatggc tcagtgggta agagcacccg actgctcttc cgaagtccag 1320
112 agttcaaaat cccagcaacc acatggtggc tcacaaccat ccgtaacaag atctgactcc 1380
113 ctcttctggt gtgtctgaag acagctacag tgtacttaca taaaataata aataaatctt 1440
114 aaaaaaaaaa aaaaaaaaa                                             1459
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121 <400> SEQUENCE: 3
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124 gttcaactcc agctatggct tcccagtgga ggtcgattct gacaccagca tcttgcagct 180
125 caaggaagtg gttgctaagc gacagggggt tccagctgac cagctgcgtg tgatttttgc 240
126 cgggaaggag cttccgaatc acctgacggt tcaaaactgt gacctggaac aacagagtat 300
127 tgtacacata gtacagagac cacggaggag aagtcatgaa acaaatgcat ctggagggga 360
128 cgaaccccag agcacctcag agggctccat atgggagtcc aggagcttga cacgagtgga 420
129 cctgagcagc cataccctgc cggtggactc tgtggggctg gcggtcattc tggacacaga 480
130 cagtaagagg gattcagaag cagccagagg tccagcagtt aaacccacct acaacagctt 540
131 tttcatctac tgcaaaggcc cctgccacaa ggtccagcct ggaaagctcc gagttcagtg 600
132 tggcacctgc aaacaagcaa ccctcacctt ggcccagggc ccatcttgct gggacgatgt 660
133 cttaattcca aaccggatga gtggtgagtg ccagtctcca gactgccctg gaaccagagc 720
134 tgaattttte tttaaatgtg gagcacaccc aacctcagac aaggacacgt cggtagcttt 780
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139 <211> LENGTH: 464
140 <212> TYPE: PRT
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147             20                  25                  30
148 Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
149         35                  40                  45
150 Glu Leu Pro Asn His Leu Thr Val Gln Asn Cys Asp Leu Glu Gln Gln
151     50                  55                  60
152 Ser Ile Val His Ile Val Gln Arg Pro Arg Arg Arg Ser His Glu Thr
153 65                  70                  75                  80
154 Asn Ala Ser Gly Gly Asp Glu Pro Gln Ser Thr Ser Glu Gly Ser Ile
155                 85                  90                  95
156 Trp Glu Ser Arg Ser Leu Thr Arg Val Asp Leu Ser Ser His Thr Leu
157             100                 105                 110
158 Pro Val Asp Ser Val Gly Leu Ala Val Ile Leu Asp Thr Asp Ser Lys
159         115                 120                 125
160 Arg Asp Ser Glu Ala Ala Arg Gly Pro Val Lys Pro Thr Tyr Asn Ser
161     130                 135                 140
162 Phe Phe Ile Tyr Cys Lys Gly Pro Cys His Lys Val Gln Pro Gly Lys
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164 Leu Arg Val Gln Cys Gly Thr Cys Lys Gln Ala Thr Leu Thr Leu Ala
165                 165                 170                 175
166 Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser
167                 180                 185                 190
168 Gly Glu Cys Gln Ser Pro Asp Cys Pro Gly Thr Arg Ala Glu Phe Phe
169             195                 200                 205
170 Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Asp Thr Ser Val Ala
171     210                 215                 220
172 Leu Asn Leu Ile Thr Ser Asn Arg Arg Ser Ile Pro Cys Ile Ala Cys
173 225                 230                 235                 240
174 Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln Cys Asn His Arg His
175                 245                 250                 255
176 Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn
177             260                 265                 270
178 Asp Arg Gln Phe Val His Asp Ala Gln Leu Gly Tyr Ser Leu Pro Cys
179         275                 280                 285
180 Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu Leu His His Phe Arg
181     290                 295                 300
182 Ile Leu Gly Glu Glu Gln Tyr Thr Arg Tyr Gln Gln Tyr Gly Ala Glu
183 305                 310                 315                 320
184 Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly Cys
185                 325                 330                 335
186 Gly Ala Gly Leu Leu Pro Glu Gln Gly Gln Arg Lys Val Thr Cys Glu
187             340                 345                 350
188 Gly Gly Asn Gly Leu Gly Cys Gly Phe Val Phe Cys Arg Asp Cys Lys
189         355                 360                 365
190 Glu Ala Tyr His Glu Gly Asp Cys Asp Ser Leu Leu Glu Pro Ser Gly
191     370                 375                 380
192 Ala Thr Ser Gln Ala Tyr Arg Val Asp Lys Arg Ala Ala Glu Gln Ala
193 385                 390                 395                 400
194 Arg Trp Glu Glu Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys Pro
195                 405                 410                 415
196 Cys Pro Arg Cys Asn Val Pro Ile Glu Lys Asn Gly Gly Cys Met His
197             420                 425                 430
198 Met Lys Cys Pro Gln Pro Gln Cys Lys Leu Glu Trp Cys Trp Asn Cys
199         435                 440                 445
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205 <211> LENGTH: 262
206 <212> TYPE: PRT
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213                 20                  25                  30
214 Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
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215           35                    40                    45
216 Glu Leu Pro Asn His Leu Thr Val Gln Asn Cys Asp Leu Glu Gln Gln
217      50                    55                    60
218 Ser Ile Val His Ile Val Gln Arg Pro Arg Arg Arg Ser His Glu Thr
219 65                    70                    75                    80
220 Asn Ala Ser Gly Gly Asp Glu Pro Gln Ser Thr Ser Glu Gly Ser Ile
221                   85                    90                    95
222 Trp Glu Ser Arg Ser Leu Thr Arg Val Asp Leu Ser Ser His Thr Leu
223              100                   105                   110
224 Pro Val Asp Ser Val Gly Leu Ala Val Ile Leu Asp Thr Asp Ser Lys
225           115                   120                   125
226 Arg Asp Ser Glu Ala Ala Arg Gly Pro Ala Val Lys Pro Thr Tyr Asn
227      130                   135                   140
228 Ser Phe Phe Ile Tyr Cys Lys Gly Pro Cys His Lys Val Gln Pro Gly
229 145                   150                   155                   160
230 Lys Leu Arg Val Gln Cys Gly Thr Cys Lys Gln Ala Thr Leu Thr Leu
231              165                   170                   175
232 Ala Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met
233              180                   185                   190
234 Ser Gly Glu Cys Gln Ser Pro Asp Cys Pro Gly Thr Arg Ala Glu Phe
235           195                   200                   205
236 Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Asp Thr Ser Val
237      210                   215                   220
238 Ala Leu Asn Leu Ile Thr Ser Asn Arg Arg Ser Ile Pro Cys Ile Ala
239 225                   230                   235                   240
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256 Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
257      35                    40                    45
258 Glu Leu Pro Asn His Leu Thr Val Gln Asn Cys Asp Leu Glu Gln Gln
259      50                    55                    60
260 Ser Ile Val His Ile Val Gln Arg Pro Arg Arg Arg Ser His Glu Thr
261 65                    70                    75                    80
262 Asn Ala Ser Gly Gly Asp Glu Pro Gln Ser Thr Ser Glu Gly Ser Ile
263                   85                    90                    95
264 Trp Glu Ser Arg Ser Leu Thr Arg Val Asp Leu Ser Ser His Thr Leu
265              100                   105                   110
266 Pro Val Asp Ser Val Gly Leu Ala Val Ile Leu Asp Thr Asp Ser Lys
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